

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/149,718

DATE: 04/26/2000
TIME: 17:59:02

INPUT SET: S35391.raw

APR 28 2000

This Raw Listing contains the General
Information Section and up to the first 5 pages.

TECH CENTER 1600/2900

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4 (i) APPLICANT: Dora K. Games, Dale B. Schenk, Lisa C. McConlogue,
5 Peter A. Seubert, and Russell E. Rydel
6 (ii) TITLE OF INVENTION: Method For Identifying Alzheimer's Disease
7 Therapeutics Using Transgenic Animal Models
8 (iii) NUMBER OF SEQUENCES: 10
9 (iv) CORRESPONDENCE ADDRESS:
10 (A) ADDRESSEE: Patrea L. Pabst
11 (B) STREET: 2800 One Atlantic Center
12 1201 West Peachtree Street
13 (C) CITY: Atlanta
14 (D) STATE: GA
15 (E) COUNTRY: USA
16 (F) ZIP: 30309-3450
17 (v) COMPUTER READABLE FORM:
18 (A) MEDIUM TYPE: Floppy disk
19 (B) COMPUTER: IBM PC compatible
20 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
21 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
22 (vi) CURRENT APPLICATION DATA:
23 (A) APPLICATION NUMBER: 09/149,718
24 (B) FILING DATE:
25 (C) CLASSIFICATION:
26 (vii) PRIOR APPLICATION DATA:
27 (A) APPLICATION NUMBER: US/08/660,487
28 (B) FILING DATE:
29
30 (A) APPLICATION NUMBER: 08/480,653
31 (B) FILING DATE: June 7, 1995
32
33 (viii) ATTORNEY/AGENT INFORMATION:
34 (A) NAME: Pabst, Patrea L.
35 (B) REGISTRATION NUMBER: 31,284
36 (C) REFERENCE/DOCKET NUMBER: ANS101CIP
37 (ix) TELECOMMUNICATION INFORMATION:
38 (A) TELEPHONE: (404)-873-8794
39 (B) TELEFAX: (404)-873-8795
40
41 (2) INFORMATION FOR SEQ ID NO:1:
42 (i) SEQUENCE CHARACTERISTICS:
43 (A) LENGTH: 2085 base pairs
44 (B) TYPE: nucleic acid
45 (C) STRANDEDNESS: double
46 (D) TOPOLOGY: linear

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47      (ii) MOLECULE TYPE: cDNA
48      (iii) HYPOTHETICAL: NO
49      (iv) ANTI-SENSE: NO
50      (ix) FEATURE:
51          (A) NAME/KEY: CDS
52          (B) LOCATION: 1-2085
53          (D) OTHER INFORMATION: /function= "coding region for APP695."
54      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
55
56      ATG CTG CCC GGT TTG GCA CTG CTC CTG CTG GCC GCC TGG ACG GCT CGG      48
57      Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
58          1              5              10              15
59
60      GCG CTG GAG GTA CCC ACT GAT GGT AAT GCT GGC CTG CTG GCT GAA CCC      96
61      Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
62          20              25              30
63
64      CAG ATT GCC ATG TTC TGT GGC AGA CTG AAC ATG CAC ATG AAT GTC CAG      144
65      Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
66          35              40              45
67
68      AAT GGG AAG TGG GAT TCA GAT CCA TCA GGG ACC AAA ACC TGC ATT GAT      192
69      Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
70          50              55              60
71
72      ACC AAG GAA GGC ATC CTG CAG TAT TGC CAA GAA GTC TAC CCT GAA CTG      240
73      Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
74          65              70              75              80
75
76      CAG ATC ACC AAT GTG GTA GAA GCC AAC CAA CCA GTG ACC ATC CAG AAC      288
77      Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
78          85              90              95
79
80      TGG TGC AAG CGG GGC CGC AAG CAG TGC AAG ACC CAT CCC CAC TTT GTG      336
81      Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
82          100             105             110
83
84      ATT CCC TAC CGC TGC TTA GTT GGT GAG TTT GTA AGT GAT GCC CTT CTC      384
85      Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
86          115             120             125
87
88      GTT CCT GAC AAG TGC AAA TTC TTA CAC CAG GAG AGG ATG GAT GTT TGC      432
89      Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
90          130             135             140
91
92      GAA ACT CAT CTT CAC TGG CAC ACC GTC GCC AAA GAG ACA TGC AGT GAG      480
93      Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
94          145             150             155             160
95
96      AAG AGT ACC AAC TTG CAT GAC TAC GGC ATG TTG CTG CCC TGC GGA ATT      528
97      Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
98          165             170             175
99

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100	GAC AAG TTC CGA GGG GTA GAG TTT GTG TGT TGC CCA CTG GCT GAA GAA	576
101	Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu	
102	180 185 190	
103		
104	AGT GAC AAT GTG GAT TCT GCT GAT GCG GAG GAG GAT GAC TCG GAT GTC	624
105	Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val	
106	195 200 205	
107		
108	TGG TGG GGC GGA GCA GAC ACA GAC TAT GCA GAT GGG AGT GAA GAC AAA	672
109	Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys	
110	210 215 220	
111		
112	GTA GTA GAA GTA GCA GAG GAG GAA GAA GTG GCT GAG GTG GAA GAA GAA	720
113	Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu	
114	225 230 235 240	
115		
116	GAA GCC GAT GAT GAC GAG GAC GAT GAG GAT GGT GAT GAG GTA GAG GAA	768
117	Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu	
118	245 250 255	
119		
120	GAG GCT GAG GAA CCC TAC GAA GAA GCC ACA GAG AGA ACC ACC AGC ATT	816
121	Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile	
122	260 265 270	
123		
124	GCC ACC ACC ACC ACC ACC ACC ACA GAG TCT GTG GAA GAG GTG GTT CGA	864
125	Ala Thr Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg	
126	275 280 285	
127		
128	GTT CCT ACA ACA GCA GCC AGT ACC CCT GAT GCC GTT GAC AAG TAT CTC	912
129	Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu	
130	290 295 300	
131		
132	GAG ACA CCT GGG GAT GAG AAT GAA CAT GCC CAT TTC CAG AAA GCC AAA	960
133	Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys	
134	305 310 315 320	
135		
136	GAG AGG CTT GAG GCC AAG CAC CGA GAG AGA ATG TCC CAG GTC ATG AGA	1008
137	Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg	
138	325 330 335	
139		
140	GAA TGG GAA GAG GCA GAA CGT CAA GCA AAG AAC TTG CCT AAA GCT GAT	1056
141	Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp	
142	340 345 350	
143		
144	AAG AAG GCA GTT ATC CAG CAT TTC CAG GAG AAA GTG GAA TCT TTG GAA	1104
145	Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu	
146	355 360 365	
147		
148	CAG GAA GCA GCC AAC GAG AGA CAG CAG CTG GTG GAG ACA CAC ATG GCC	1152
149	Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala	
150	370 375 380	
151		
152	AGA GTG GAA GCC ATG CTC AAT GAC CGC CGC CGC CTG GCC CTG GAG AAC	1200

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153	Arg	Val	Glu	Ala	Met	Leu	Asn	Asp	Arg	Arg	Arg	Leu	Ala	Leu	Glu	Asn	
154	385					390					395					400	
155																	
156	TAC	ATC	ACC	GCT	CTG	CAG	GCT	GTT	CCT	CCT	CGG	CCT	CGT	CAC	GTG	TTC	1248
157	Tyr	Ile	Thr	Ala	Leu	Gln	Ala	Val	Pro	Pro	Arg	Pro	Arg	His	Val	Phe	
158					405				410						415		
159																	
160	AAT	ATG	CTA	AAG	AAG	TAT	GTC	CGC	GCA	GAA	CAG	AAG	GAC	AGA	CAG	CAC	1296
161	Asn	Met	Leu	Lys	Lys	Tyr	Val	Arg	Ala	Glu	Gln	Lys	Asp	Arg	Gln	His	
162				420				425					430				
163																	
164	ACC	CTA	AAG	CAT	TTC	GAG	CAT	GTG	CGC	ATG	GTG	GAT	CCC	AAG	AAA	GCC	1344
165	Thr	Leu	Lys	His	Phe	Glu	His	Val	Arg	Met	Val	Asp	Pro	Lys	Lys	Ala	
166			435					440					445				
167																	
168	GCT	CAG	ATC	CGG	TCC	CAG	GTT	ATG	ACA	CAC	CTC	CGT	GTG	ATT	TAT	GAG	1392
169	Ala	Gln	Ile	Arg	Ser	Gln	Val	Met	Thr	His	Leu	Arg	Val	Ile	Tyr	Glu	
170		450				455					460						
171																	
172	CGC	ATG	AAT	CAG	TCT	CTC	TCC	CTG	CTC	TAC	AAC	GTG	CCT	GCA	GTG	GCC	1440
173	Arg	Met	Asn	Gln	Ser	Leu	Ser	Leu	Leu	Tyr	Asn	Val	Pro	Ala	Val	Ala	
174	465				470					475					480		
175																	
176	GAG	GAG	ATT	CAG	GAT	GAA	GTT	GAT	GAG	CTG	CTT	CAG	AAA	GAG	CAA	AAC	1488
177	Glu	Glu	Ile	Gln	Asp	Glu	Val	Asp	Glu	Leu	Leu	Gln	Lys	Glu	Gln	Asn	
178				485				490						495			
179																	
180	TAT	TCA	GAT	GAC	GTC	TTG	GCC	AAC	ATG	ATT	AGT	GAA	CCA	AGG	ATC	AGT	1536
181	Tyr	Ser	Asp	Asp	Val	Leu	Ala	Asn	Met	Ile	Ser	Glu	Pro	Arg	Ile	Ser	
182			500					505					510				
183																	
184	TAC	GGA	AAC	GAT	GCT	CTC	ATG	CCA	TCT	TTG	ACC	GAA	ACG	AAA	ACC	ACC	1584
185	Tyr	Gly	Asn	Asp	Ala	Leu	Met	Pro	Ser	Leu	Thr	Glu	Thr	Lys	Thr	Thr	
186			515					520				525					
187																	
188	GTG	GAG	CTC	CTT	CCC	AGC	CTG	GAC	GAT	CTC	CAG	CCG	TGG	CAT	TCT	TTT	1632
189	Val	Glu	Leu	Leu	Pro	Val	Asn	Gly	Glu	Phe	Ser	Leu	Asp	Asp	Leu	Gln	
190		530				535					540						
191																	
192	GTG	AAT	GGA	GAG	TTC	GGG	GCT	GAC	TCT	GTG	CCA	GCC	AAC	ACA	GAA	AAC	1680
193	Pro	Trp	His	Ser	Phe	Gly	Ala	Asp	Ser	Val	Pro	Ala	Asn	Thr	Glu	Asn	
194	545				550					555					560		
195																	
196	GAA	GTT	GAG	CCT	GTT	GAT	GCC	CGC	CCT	GCT	GCC	GAC	CGA	GGA	CTG	ACC	1728
197	Glu	Val	Glu	Pro	Val	Asp	Ala	Arg	Pro	Ala	Ala	Asp	Arg	Gly	Leu	Thr	
198				565				570						575			
199																	
200	ACT	CGA	CCA	GGT	TCT	GGG	TTG	ACA	AAT	ATC	AAG	ACG	GAG	GAG	ATC	TCT	1776
201	Thr	Arg	Pro	Gly	Ser	Gly	Leu	Thr	Asn	Ile	Lys	Thr	Glu	Glu	Ile	Ser	
202			580					585					590				
203																	
204	GAA	GTG	AAG	ATG	GAT	GCA	GAA	TTC	CGA	CAT	GAC	TCA	GGA	TAT	GAA	GTT	1824
205	Glu	Val	Lys	Met	Asp	Ala	Glu	Phe	Arg	His	Asp	Ser	Gly	Tyr	Glu	Val	

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	595	600	605	
206				
207				
208	CAT CAT CAA AAA TTG GTG TTC TTT GCA GAA GAT GTG GGT TCA AAC AAA			1872
209	His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys			
210	610	615	620	
211				
212	GGT GCA ATC ATT GGA CTC ATG GTG GGC GGT GTT GTC ATA GCG ACA GTG			1920
213	Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val			
214	625	630	635	640
215				
216	ATC GTC ATC ACC TTG GTG ATG CTG AAG AAG AAA CAG TAC ACA TCC ATT			1968
217	Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile			
218	645	650	655	
219				
220	CAT CAT GGT GTG GTG GAG GTT GAC GCC GCT GTC ACC CCA GAG GAG CGC			2016
221	His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg			
222	660	665	670	
223				
224	CAC CTG TCC AAG ATG CAG CAG AAC GGC TAC GAA AAT CCA ACC TAC AAG			2064
225	His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys			
226	675	680	685	
227				
228	TTC TTT GAG CAG ATG CAG AAC			2085
229	Phe Phe Glu Gln Met Gln Asn			
230	690	695		
231				
232	(2) INFORMATION FOR SEQ ID NO:2:			
233	(i) SEQUENCE CHARACTERISTICS:			
234	(A) LENGTH: 695 amino acids			
235	(B) TYPE: amino acid			
236	(D) TOPOLOGY: linear			
237	(ii) MOLECULE TYPE: protein			
238	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:			
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240	Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg			
241	1	5	10	15
242				
243	Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro			
244	20	25	30	
245				
246	Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln			
247	35	40	45	
248				
249	Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp			
250	50	55	60	
251				
252	Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu			
253	65	70	75	80
254				
255	Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn			
256	85	90	95	
257				
258	Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val			

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/149,718

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Original Text